

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/965536

Source: OIPE

Date Processed by STIC: 11/07/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/965536
ATTN: NEW RULES CASES: PLEASE DISREGARD ENCLISII "ALPIIA" HEADERS, WHICH WERE INSERTED BY P		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino <input type="checkbox"/> Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-.<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-.<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-.<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID.NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's <input type="checkbox"/> (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-.<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents	
10 <input type="checkbox"/> Invalid <213> <input type="checkbox"/> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-.<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/965,536

DATE: 11/07/2001
TIME: 14:48:12

Input Set : A:\30534111.app
Output Set: N:\CRF3\11072001\I965536.raw

3 <110> APPLICANT: FEDER, J. N.
 4 MINTIER, G.
 5 RAMANATHAN, C. S.
 6 HAWKEN, D. R.
 8 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY5,
 9 EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
 11 <130> FILE REFERENCE: D0041NP/3053-4118US3
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/965,536 08
 14 <141> CURRENT FILING DATE: 2001-09-26
 16 <150> PRIOR APPLICATION NUMBER: 60/235,713
 17 <151> PRIOR FILING DATE: 2000-09-27
 19 <150> PRIOR APPLICATION NUMBER: 60/261,781
 20 <151> PRIOR FILING DATE: 2001-01-16
 22 <150> PRIOR APPLICATION NUMBER: 60/306,605
 23 <151> PRIOR FILING DATE: 2001-07-19
 25 <150> PRIOR APPLICATION NUMBER: 60/310,436
 26 <151> PRIOR FILING DATE: 2001-08-03
 28 <160> NUMBER OF SEQ ID NOS: 61
 30 <170> SOFTWARE: PatentIn Ver. 2.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 2214
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
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 40 tgcttacccc gagctttca ctgtgtggc aaggatgact gtgggaacgg ggcggacgaa 180
 41 gagaactgtg gtgacactag tggatggggc accatatttg gcacagtgc tggaaatgct 240
 42 aacagcgtgg ccttaacaca ggagtgcctt ctaaaacagt atccacaatg ctgtgactgc 300
 43 aaagaaaactg aatttggatg tgtaaatggt gacttaaagt ctgtgccat gatttctaac 360
 44 aatgtgacat tactgtctct taagaaaaac aaaatccaca gtcttccaga taaagtttc 420
 45 atcaaataca caaaaacttaa aaagatattt cttcagcata attgcattag acacatatcc 480
 46 agggaaagcat tttttggatt atgtaatctg caaatattat atctcaacca caactgcac 540
 47 acaaccctca gacctggaat attcaaagac ttacatcagc taacttgggt aattcttagat 600
 48 gacaatccaa taaccagaat ttacacgcgc ttgtttacgg gattaaattc cttgttttc 660
 49 ctgtctatgg ttaataacta cttagaagct cttcccaagc agatgtgtgc ccaaatgcct 720
 50 caactcaact gggggattt ggaaggcaat agaataaaagt atctcacaaa ttctacgttt 780
 51 ctgtcgtgcg attcgctcac agtgctgttt ctgccttagaa atcaaattgg ttttgcattca 840
 52 gagaagacat tttcttcatt aaaaaattta ggagaactgg atctgtctag caatacgata 900
 53 acggagctat cacctcacct ttttaaagac ttgaagcttc tacaaaagct gaacctgtca 960
 54 tccaaatccctc ttatgtatct tcacaagaac cagttgaaa gtcttaaaca acttcagtct 1020
 55 ctagacctgg aaaggataga gattccaaat ataaacacac gaatgtttca acccatgaag 1080
 56 aatctttctc acatttattt caaaaacttt cgatactgct cctatgctcc ccatgtccga 1140
 57 atatgtatgc ccttgacggc cggcatttct tcatttgagg acctcttggc taacaatatac 1200
 58 ctcagaatat ttgtctgggt tatagctttc attacctgct ttggaaatct ttttgcattt 1260
 59 ggcatgagat ctttcattaa agctgaaaaat acaactcagc ctatgtccat caaaatcctt 1320
 60 tggcgtctg attgcctgat ggggtttac ttgttcttg ttggcatttt cgatataaaa 1380

Erroneous:
 check above
 for 21 and 22
 for 21 and 22

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 62 atggggttcc tggccatgct gtccaccgaa gtctctgttc tgctactgac ctacttgact 1500
 63 ttggagaagt tcctgtcat tgtcttcccc ttcaactaaca ttgcacctgg aaaacggcag 1560
 64 acctcagtca tcctcatttg catctggatg gcgggatttt taatagctgt aattccattt 1620
 65 tggaaataagg attatttgg aaacttttat gggaaaaatg gagtatgtt cccactttat 1680
 66 tatgaccaaa cagaagatata tggaaagcaaa gggattctc ttggaaattt cctaggtgt 1740
 67 aacttgctgg cttttctcat cattgtgtt tcctatatta ctatgttctg ttccattcaa 1800
 68 aaaaccgcct tgcagaccac agaagtaagg aattgttttgaagagaggt ggctgttgca 1860
 69 aatcggttct tttttatagt gttctctgtat gccatctgct ggattcctgtt atttgttagtt 1920
 70 aaaatcctt ccctcttccg ggtggaaata ccagacacaa tgacttcctg gatagtgatt 1980
 71 ttttccttc cagttAACAG tgctttgaat ccaatcctct atactctcac aaccacattt 2040
 72 tttaaggaca agttgaaaca gctgctgcac aaacatcaga ggaatcaat ttcaaaattt 2100
 73 aaaaaaaaaaa gtttatctac atccattgtt tggatagagg actcctcttc cctgaaactt 2160
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 79 <212> TYPE: PRT
 80 <213> ORGANISM: Homo sapiens
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 84 1 5 10 15
 85 Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr
 86 20 25 30
 87 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
 88 35 40 45
 89 Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
 90 50 55 60
 91 Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala
 92 65 70 75 80
 93 Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln
 94 85 90 95
 95 Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu
 96 100 105 110
 97 Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys
 98 115 120 125
 99 Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr
 100 130 135 140
 101 Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser
 102 145 150 155 160
 103 Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn
 104 165 170 175
 105 His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His
 106 180 185 190
 107 Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser
 108 195 200 205
 109 Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val
 110 210 215 220
 111 Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro
 112 225 230 235 240

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128 Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr
129 245 250 255
131 Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu Pro
132 260 265 270
134 Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys
135 275 280 285
137 Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser
138 290 295 300
140 Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu Ser
141 305 310 315 320
143 Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu Lys
144 325 330 335
146 Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Asn
147 340 345 350
149 Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys
150 355 360 365
152 Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met Pro
153 370 375 380
155 Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn Ile
156 385 390 395 400
158 Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly Asn
159 405 410 415
161 Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr
162 420 425 430
164 His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly
165 435 440 445
167 Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly Gln
168 450 455 460
170 Tyr Gln Lys Tyr Ala Leu Trp Met Glu Ser Val Gln Cys Arg Leu
171 465 470 475 480
173 Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu
174 485 490 495
176 Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser
177 500 505 510
179 Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys Ile
180 515 520 525
182 Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys Asp
183 530 535 540
185 Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr
186 545 550 555 560
188 Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly Ile
189 565 570 575
191 Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser Tyr
192 580 585 590
194 Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu
195 595 600 605
197 Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val Ala Asn Arg Phe Phe
198 610 615 620
200 Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val

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Input Set : A:\30534111.app
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201 625 630 635 640
 203 Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr Ser
 204 645 650 655
 206 Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile
 207 660 665 670
 209 Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu
 210 675 680 685
 212 Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser
 213 690 695 700
 215 Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu
 216 705 710 715 720
 218 Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val
 219 725 730 735
 221 Ser
 225 <210> SEQ ID NO: 3
 226 <211> LENGTH: 17
 227 <212> TYPE: DNA
 228 <213> ORGANISM: Homo sapiens
 230 <400> SEQUENCE: 3
 231 ccacgcgtcc gattaca 17
 234 <210> SEQ ID NO: 4
 235 <211> LENGTH: 1026
 236 <212> TYPE: DNA
 237 <213> ORGANISM: Homo sapiens
 239 <400> SEQUENCE: 4
 240 caatcatttt ggatcactgg actttcagtg gactacctaa aacaggggac agcttttgg 60
 241 agatgacatc tgcaatgctt ttcatcttta ccaacggcaa gccttctgc acagagagca 120
 242 cagcagaatg gtcctgtca ctgcattcca atggcagctg tactatctac caaccgtgct 180
 243 gaggacagca ccaaagggtc ctctcctcac cccacatgcc tgaaaagcac atgtgaattc 240
 244 gtgtatagtg ggctgaggtg cagctgatct cttagtatac aacacaaccc accaacaat 300
 245 gaccacaggt tggcaactgtg tggctttca catcggttg cactgtccat gaaatagaaa 360
 246 cactcacaac atctgattcc agtgtggcca taataacaga aatctaacaa ctcttcctt 420
 247 gcctttcaa tatcaaataa aaccatcagc atcctgctgg attgatagca aaggatttcc 480
 248 aaaatattca tctacccgaa gtcctcctt gtgaaggccg gtggagtagc cactttgaaa 540
 249 acagaacttc caaccagggtt accatgtcta acctatgacc agagagtac actgatgaag 600
 250 cctcataccca tttgcctttt ggattttatt taatatcaga agagatgaat tcttaagata 660
 251 ttttctgaa ggttgcggcag ggcacaaaaca aattggacac tttcactgct aaaaagtaca 720
 252 cttaaatatt cttaaagtat aatttcttta gagcagtatc cctattgctg gcaagttctg 780
 253 ctttcataaaa atatgcagat aagaagtgtt aaatgggatt caagaattat gtttttattt 840
 254 gggactgttt gcataactcac aatggtttg ttctcattgt ttttaacaaa aaagcaatga 900
 255 agtttgggtt ggtttttga aaacgaaact gaaaaaaatt atatgtaaaa atgagaactg 960
 256 ggttaaataaaa attatatttt gcaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
 257 aaaaag 1026
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 261 <211> LENGTH: 2142
 262 <212> TYPE: DNA
 263 <213> ORGANISM: Homo sapiens
 265 <400> SEQUENCE: 5
 266 atgttcttca tacttcattt catcggtctg atcaatgtca aagattttgc actgactcaa 60

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Input Set : A:\30534111.app
Output Set: N:\CRF3\11072001\I965536.raw

267 ggttagcatga tcactccttc atgccaaaaa ggatatttc cctgtggaa tcttaccaag 120
 268 tgcttacccc gagctttca ctgtgatgc aaggatgact gtggAACGG ggcggacgaa 180
 269 gagaactgtg gtgacactag tggatggcg accatatttgc acagtgc tggaaatgt 240
 270 aacacgtgg ccttaacaca ggagtgcctt ctaaaacagt atccacaatgc ctgtgactgc 300
 271 aaagaaactg aatttggaaatgt tgtaaatgtt gacttaaagt ctgtggcgat gatttcta 360
 272 aatgtgacat tactgtctc taagaaaaac aaaatccaca gtctccaga taaagtttc 420
 273 atcaaataca caaaacttaa aaagatattt ctcagcata attgcattt acacatatcc 480
 274 agggaaagcat ttttggatt atgtaatctg caaatattaa ttctagatga caatccaata 540
 275 accagaattt cacagcgctt gtttacggaa ttaaatttctt tggttttctt gtctatgg 600
 276 aataactact tagaagctct tcccaagcag atgtgtgc 660
 277 gtggatttgg aaggcaatag aataaagtat ctcacaaattt ctacgtttctt gtctgtcgat 720
 278 tgcgtcacag tgctgtttctt gccttagaaat caaatttggtt ttgttccaga gaagacattt 780
 279 tcttcattaa aaaattttagg agaactggat ctgtctagca atacgataac ggagctatca 840
 280 cctcacctt ttaaagactt gaagcttcta caaaagctga acctgtcatc caatccctt 900
 281 atgtatctt acaagaacca gtttggaaatg cttaaacaac ttctagatctt agacctggaa 960
 282 aggatagaga ttccaaatataa aacacacaga atgttcaac ccatgaaagaa tctttctcac 1020
 283 atttatttca aaaacttctg atactgtctc tatgtccccc atgtccgaat atgtatgc 1080
 284 ttgacggacgc gcatttcttctt atttgaggac ctcttggctt acaatatctt cagaatattt 1140
 285 gtctgggtta tagcttcat tacctgctt ggaaatctt ttgtcatttgc catgagatct 1200
 286 ttcatattaaatctg ctgaaaatac aactcacgtt atgtccatca aaatcccttgc ttgtgtgt 1260
 287 tgccgtatgg gtgtttactt gtttgcgtt ggcattttcg atataaaaata ccgaggcc 1320
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 289 gccatgctgtt ccacccaaatgtt ctctgttctg ctactgacactt acttgactt ggagaagttc 1440
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 291 ctcatttgc tctggatggc gggatttttta atagctgtaa ttccatatttgc gaataaggat 1560
 292 tattttggaa acttttatgg gaaaaatggaa gtatgtttcc cacttttataa tgaccaaaca 1620
 293 gaagatatttgc gaagccaaagg gtatttctt ggaattttcc taggtgtgaa cttgtgtgg 1680
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 295 cagaccacacaaatgtt aacttgcgtt gggatggatggag aacgtgcgtt gccgcctcat 1800
 296 ttatataatgtt tctctgtatgc catctgcttgc attccctgtat ttgtgtttaa aatcccttcc 1860
 297 ctcttcgggg tggaaatacc agacacaatg acttccgttgc tagtgcattt tttcccttcca 1920
 298 gtaacagtg ctgttgcatttca aatcccttgcacttgcataa ccaactttttaaaggacaag 1980
 299 ttgaaacacgc tgctgcacaa acatcagagg aaatcaattt tcaaaattttaa aaaaaaaatgtt 2040
 300 ttatctacat ccatttgcgtt gatagaggac tcctcttccc tggaaacttgg ggttttgcac 2100
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 304 <210> SEQ ID NO: 6
 305 <211> LENGTH: 713
 306 <212> TYPE: PRT
 307 <213> ORGANISM: Homo sapiens
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 314 20 25 30
 316 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
 317 35 40 45
 319 Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
 320 50 55 60
 322 Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala

09965536

<210> 29
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo 1;
 N=A+G+C+T; K=C+G+T

<400> 29

cgaagcgtaa gggcccagcc ggcnnknnk nnknnknnkn nknnknnknn knnknnknnk 60
 nnknnknnkn nnnnknnkn knnkccgggt cggggcggc 99

<210> 30
 <211> 95
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo 2;
 N=A+G+C+T; V=C+A+G

<400> 30

aaaagggaaaa aagcgccgc vnnvnnvnnv nnvnnvnnv nvnnvnnvnn vnnvnnvnnv 60
 nnvnnvnnvn vnnvnnvnn gccgccccga cccgg 95

Does Not Comply
 Corrected Diskette Needed

Must enumerate unknowns "n's" in
 fields 221, 222 and 223.

met

Fields 221 and 222 must be included in addition
 to fields 223. Unknowns must be enumerated as
 follows: "unrec", some numeric location, and some
 possible value.

Notation is odd. Do you mean
more clearly That $N = A \underline{\underline{or}} G \underline{\underline{or}} C \underline{\underline{or}} T$

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/965,536

DATE: 11/07/2001

TIME: 14:48:13

Input Set : A:\30534111.app

Output Set: N:\CRF3\11072001\I965536.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1767 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:1767 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1768 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:1768 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:1768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1781 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1781 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1782 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1782 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30